

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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(ii) TITLE OF INVENTION: AVIAN GHD GENES AND THEIR USE IN METHODS FOR
SEX IDENTIFICATION IN BIRDS

(iii) NUMBER OF SEQUENCES: 39

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: WO PCT/GB96/01341

(B) FILING DATE: 05-JUN-1996

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9511439.3

(B) FILING DATE: 06-JUN-1995

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(F) ZIP: 20006

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 263/PPNTIR1172US

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 723 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCGGTCGGA GGTTC AAGG AATGACTAGA TGTGGCACTT AGTGCCATGG TCTAGTTGAC	60
AAGGTGATGG TTGGTCAAAA GTTGGACTCG ATGATCTCAG AGTTTTTTTTC CAGCCTTAAT	120
AATTCTATGA ATTCTGTAAT TTTATTCTTG ATCTTTTTTGA GCGAAGTTTG TTTGGGGATT	180
TTAGTTTGGT TTCCCTGTCA CTGTTTTCTT TCCTTGAAAC TGACTTTCAT TTGCAACATG	240
AGAATTGCTG TATTTGTCAG GTTACAAGTA GTGCAATGGC TGCTTAGAAG TAGTGAGAAA	300
CATTTAGGGA AATACTGGAG TGAAGCAAAC ACAGTGGTAC TGCCAAACTG TAGCTTTGGG	360
ATTTGAGGAG CCACAGAGTT GTATATAAAT TTGTTTAATG ATATCCTGCC CCTGCCTTCC	420
ATTAATTGCT TGTTTTATGA AACCACTCTT TTTTTTTTTT TTTTTTTTTT GGCTTCTTCA	480
TATCCTGTGG TAATGAGTTA ATGCATTTAG AAGCACATGG CAGAACTAGG AGATCTGTGG	540
ATGACAGTGG TACAGGAGCT CTGAATTTTT TAGATAAACT ATGAGAGTGG AAACAGAAAT	600
CTGAGGCTAG TTTCTTGAGC TGACTGTAAA TTTTGTGAGA ATATTTTCAA GACTACATTA	660
GTTGTGTGTT TGAGGAAAAA TAAAATGTTT AAGTTGTCCA TTCCTTGAAA CCTCCCGACC	720
GGG	723

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATTCTTCCAG ATGATCCTGA TAAAAAACCA CAAGCAAAAC AGTTACAGAC CAAAAAACCA	60
CAAGCAAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA AACTACTTAG CAGAGATCTT	120
GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG	153

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAAGC AGCTACAGAC CAAGAAACCC	60
CAGGCAAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA AATTACTGAA TAAAGACCTT	120
GCAAGAAAGG AAGCACAAAG GCTTGCTGGT GCA	153

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC CAAGAAACCC	60
CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT	120
GCAAGAAAGG AAGCACAGAG ACTTGCTGGT GCA	153

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAAGC AGTTGCAGAC CAAGAAACCA	60
CAGGCAAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA AATTACTGAA TAAAGACCTT	120
GCAAGAAAAG AAGTGCAAAG ACTTACTGGT GCA	153

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Ile Leu Pro Asp Asp Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln

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1	5	10	15												
Thr	Arg	Ala	Asp	Tyr	Leu	Ile	Lys	Leu	Leu	Ser	Arg	Asp	Leu	Ala	Lys
	20						25						30		
Arg	Glu	Ala	Gln	Arg	Leu	Cys	Gly	Ala							
	35						40								

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ile	Leu	Pro	Asp	Asp	Pro	Asp	Lys	Lys	Pro	Gln	Ala	Lys	Gln	Leu	Gln
1					5				10					15	
Thr	Arg	Ala	Asp	Tyr	Leu	Ile	Lys	Leu	Leu	Asn	Lys	Asp	Leu	Ala	Arg
			20						25				30		
Lys	Glu	Ala	Gln	Arg	Leu	Ala	Gly	Ala							
			35						40						

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ile	Leu	Pro	Asp	Asp	Pro	Asp	Lys	Lys	Pro	Gln	Ala	Lys	Gln	Leu	Gln
1				5					10					15	
Thr	Arg	Ala	Asp	Tyr	Leu	Ile	Lys	Leu	Leu	Asn	Lys	Asp	Leu	Ala	Arg
				20					25					30	
Lys	Glu	Ala	Gln	Arg	Leu	Ala	Gly	Ala							
				35					40						

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ile	Leu	Pro	Asp	Asp	Pro	Asp	Lys	Lys	Pro	Gln	Ala	Lys	Gln	Leu	Gln
1				5					10					15	
Thr	Arg	Ala	Asp	Tyr	Leu	Ile	Lys	Leu	Leu	Asn	Lys	Asp	Leu	Ala	Arg
				20					25					30	
Lys	Glu	Val	Gln	Arg	Leu	Thr	Gly	Ala							
				35					40						

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6608 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG AAGGCCTGGC	60
CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT TGGCCATCTG TAGAGAATAG	120
CAAGTCAAAC GCATTACTTC GAAAACATAC GGAGTACCAG AAAGGGGATT CTTGACCTAC	180
ACCTTGTAAC CTGAGTGGAC TTTCTTTTTA ACTTCTTAAT ACTTACAATG AATGGGCACA	240
GTGATGAAGA AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG	300
GGTCAGCTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT GGAAGTAGCA	360
GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC AGGCAGTCAA TCCGAATCAG	420
AGTCTGACAC ATCTAGAGAG AAGAAACAAG TTCAAGCTAA ACCTCCGAAA GCTGACGGAT	480
CTGAGTTTTG GAAGTCCAGT CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA	540
AGCAACAGCA ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA	600
GTAGTGAAGA TTCTGCCGAT GATTCGTCCA GTGAAACTAA GAAGAAAAAG CATAAAGATG	660
AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC TGGTTCTGAT TCTGAATCGG	720
CGGAAGATGG GGATAAAAGC AGTTGTGAAG AAAGTGAATC TGACTATGAG CCAAAAAACA	780
AAGTCAAAAG CCGTAAACCT CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG	840
GACAGAAGAA GAGGCAACTT GATTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG	900
ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA GCTGAAGAAA	960
CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA GGATGTCCCA CAGACTGAAG	1020

AAGATGAATT	TGAAACTATA	GAGAAGTTTA	TGGACAGTCG	AATTGGCCGA	AAAGGAGCCA	1080
CTGGTGCCTC	AACCACCATC	TATGCCGTTG	AGGCAGATGG	TGACCCAAAT	GCTGGGTTTG	1140
AAAAGTCAAA	GGAGCTGGGA	GAAATACAGT	ATCTTATTAA	ATGGAAAGGC	TGGTCACACA	1200
TCCATAACAC	TTGGGAAACT	GAAGAAACGC	TGAAGCAACA	AAATGTTAAA	GGAATGAACA	1260
AACTGGACAA	CTACAAGAAA	AAGGATCAGG	AGACAAAACG	CTGGCTGAAA	AATGCTTCTC	1320
CAGAAGATGT	GGAATATTAT	AACTGCCAGC	AGGAGCTTAC	AGATGATCTG	CACAAACAAT	1380
ATCAAATAGT	GGAAAGAATA	ATTGCTCATT	CAAATCAAAA	GTCAGCAGCT	GGTTATCCGG	1440
ACTACTATTG	CAAATGGCAG	GGTCTGCCTT	ACTCAGAATG	TAGCTGGGAA	GATGGTGCTC	1500
TCATTGCCAA	AAAGTTTCAG	GCACGCATTG	ATGAGTATTT	TAGCAGAAAT	CAATCCAAGA	1560
CTACTCCCTT	TAAGGACTGC	AAGGTCTAA	AACAGAGACC	AAGATTTGTT	GCACTGAAGA	1620
AGCAACCATC	TTACATTGGA	GGACATGAAA	GTCTGGAGTT	AAGAGATTAT	CAGTTAAATG	1680
GATTGAATTG	GCTCGCTCAT	TCATGGTGCA	AAGGAAATAG	TTGTATTCTT	GCAGATGAAA	1740
TGGGTCTGGG	TAAAACAATA	CAAACAATTT	CTTTTCTGAA	CTACCTGTTT	CATGAACATC	1800
AACTGTATGG	CCCTTTTCTT	CTGCGCGTGC	CACTTTCTAC	CTTGACATCT	TGGCAAAGAG	1860
AGATTCAAAC	TTGGGCTCCT	CAGATGAATG	CTGTAGTTTA	CTTAGGAGAT	ATAACTAGTA	1920
GAAATATGAT	AAGGACTCAT	GAATGGATGC	ATCCACAGAC	TAAACGATTA	AAGTTTAACA	1980
TACTTCTGAC	GACATATGAA	ATTTTACTGA	AGGATAAGTC	ATTCCTTGGT	GGTCTCAATT	2040
GGGCATT CAT	AGGAGTTGAT	GAAGCTCATC	GTTTAAAAAA	TGATGACTCT	CTTCTGTACA	2100
GGACTTTAAT	AGACTTTAAG	TCCAACCATC	GACTTCTGAT	TACTGGAACC	CCACTGCAAA	2160
ATTCCCTCAA	AGAGCTGTGG	TCTTTGTTGC	ATTTCATCAT	GCCAGAAAAA	TTTTCTCCT	2220
GGGAAGATTT	TGAAGAGGAG	CATGGCAAAG	GAAGAGAGTA	TGGTTATGCA	AGTCTTCACA	2280
AAGAGCTTGA	ACCATTTTTA	CTAAGAAGAG	TTAAAAAAGA	TGTAGAAAAG	TCTTTACCTG	2340
CTAAGGTTGA	ACAAATTCTG	AGGATGGAAA	TGAGTGCATT	GCAGAAGCAA	TATTACAAGT	2400
GGATTTTAAC	AAGGAATTAT	AAAGCCCTCA	GTAAAGGTTT	AAAAGGCAGT	ACCTCAGGCT	2460
TTCTGAACAT	TATGATGGAA	CTTAAGAAGT	GTTGTAACCA	TTGCTACCTC	ATTAAGCCAC	2520

CAGATGATAA	TGAATTCTAT	AATAAACAGG	AGGCCTTACA	GCATTTGATA	CGTAGCAGCG	2580
GGAAACTAAT	CCTTCTTGAC	AAGCTACTGA	TTCGTCTGCG	AGAACGTGGC	AACAGAGTTC	2640
TGATTTTCTC	TCAGATGGTG	AGGATGCTGG	ACATCCTAGC	AGAATATCTG	AAGTATCGCC	2700
AGTTTCCCTT	CCAGAGACTT	GATGGATCAA	TAAAAGGGGA	ATTGAGGAAG	CAAGCACTGG	2760
ATCATTTCAA	TGCAGAAGGA	TCAGAGGATT	TCTGTTTTTT	ACTGTCTACA	AGAGCTGGAG	2820
GATTAGGTAT	TAACTTGGCA	TCTGCTGACA	CTGTAGTTAT	TTTTGATTCT	GACTGGAATC	2880
CACAGAATGA	TCTGCAGGCA	CAGGCGAGAG	CTCATAGAAT	TGGACAGAAG	AAACAGGTTA	2940
ATATTTATCG	GCTAGTCACA	AAAGGATCAG	TAGAAGAAGA	TATTCTTGAA	AGAGCCAAGA	3000
AGAAGATGGT	GCTAGACCAT	TTAGTAATTC	AGAGAATGGA	CACGACAGGA	AAAACGTGTC	3060
TGCATACAGG	TTCAACTCCA	TCAAGCTCTA	CACCTTTTAA	TAAAGAAGAG	TTATCAGCTA	3120
TTTTGAAGTT	TGGTGCTGAG	GAACCTTTTA	AAGAACCTGA	AGGAGAAGAA	CAGGAGCCCC	3180
AGGAAATGGA	TATAGATGAA	ATCTTGAAGA	GAGCTGAAAC	TCGGGAAAAT	GAGCCAGGTC	3240
CATTGACTGT	AGGGGATGAG	TTGCTTTCAC	AGTTCAAGGT	GGCGAACTTT	TCCAATATGG	3300
ATGAAGATGA	TATTGAGTTG	GAACCAGAAA	GAAATTCAAG	AAATTGGGAA	GAAATCATCC	3360
CAGAATCCCA	ACGGAGAAGG	ATAGAGGAGG	AGGAAAGACA	AAAAGAACTT	GAAGAAATAT	3420
ACATGCTCCC	GAGGATGAGA	AACTGTGCAA	AACAGATCAG	CTTTAATGGG	AGTGAAGGAA	3480
GACGCAGTAG	GAGCAGAAGA	TATTCTGGAT	CTGATAGTGA	CTCCATCACA	GAAAGAAAAC	3540
GGCCAAAAAA	GCGTGGAAGA	CCTCGAACCA	TTCCTCGAGA	AAATATTAAA	GGATTTAGTG	3600
ATGCAGAGAT	CAGGCGGTTT	ATCAAGAGTT	ACAAGAAATT	TGGTGGCCCT	CTGGAAAGGT	3660
TAGATGCTGT	AGCTAGAGAT	GCTGAACTGG	TTGATAAATC	TGAGACAGAC	CTTAGACGTT	3720
TGGGTGAACT	TGTACATAAT	GGATGCATTA	AGGCTTTAAA	GGACAATTCA	TCTGGACAAG	3780
AAAGAGCAGG	AGGTAGACTT	GGGAAAGTTA	AAGGCCCAAC	GTTTCGAATC	TCAGGAGTGC	3840
AGGTGAATGC	AAAAC TAGTC	ATCTCTCACG	AAGAAGAGCT	GGCACC ACTG	CACAAATCCA	3900
TTCCTTCAGA	TCCAGAAGAA	AGGAAAAGAT	ATGTCATCCC	ATGCCACACC	AAGGCTGCTC	3960
ACTTCGATAT	AGATTGGGGT	AAAGAAGATG	ATTCCAATCT	GTTAGTAGGC	ATCTATGAAT	4020

ATGGCTATGG	CAGCTGGGAA	ATGATAAAAA	TGGATCCAGA	TCTCAGCTTA	ACACAGAAGA	4080
TTTTACCTGA	TGATCCAGAC	AAGAAACCCC	AGGCAAAGCA	GCTACAGACC	CGTGCAGACT	4140
ACCTCATTA	ATTACTGAAT	AAAGACCTTG	CAAGAAAGGA	AGCACAAAGG	CTTGCTGGTG	4200
CAGGCAATTC	CAAGAGAAGG	AAGACAAGAA	ATAAGAAGAA	TAAGATGAAG	GCTTCAAAAA	4260
TAAAAGAAGA	AATAAAGAGT	GATTCTTCAC	CACAACCCTC	AGAAAAATCT	GATGAAGATG	4320
ATGAGGAGGA	GGATAACAAG	GTAAATGAAA	TGAAATCTGA	AAATAAAGAA	AAATCTAAAA	4380
AAATTCCATT	GCTGGATACT	CCAGTTCATA	TTACTGCAAC	CAGTGAACCA	GTCCTATCT	4440
CAGAAGAATC	TGAAGAACTC	CATCAGAAGA	CATTTAGTGT	GTGCAAAGAA	AGAATGAGGC	4500
CTGTCAAAGC	AGCACTGAAA	CAGCTGGATA	GACCAGAGAA	GGGCCTTTCT	GAAAGGGAGC	4560
AGCTGGAACA	TACTAGGCAG	TGTCTAATCA	AAATTGGGGA	TCACATTACA	GAATGCCTGA	4620
AGGAGTACAC	AAATCCCGAG	CAAATAAAAC	AGTGGAGGAA	AAATTTGTGG	ATTTTTGTGT	4680
CCAAGTTTAC	AGAATTTGAT	GCCAGAAAGC	TGCACAAACT	CTACAAACAT	GCAATCAAAA	4740
AGCGCCAAGA	GTCTCAGCAA	CACAATGACC	AAAACATTAG	CAGCAATGTG	AATACACATG	4800
TAATCAGAAA	TCCAGATGTG	GAAAGACTGA	AGGAGACTAC	AAACCATGAT	GATAGTAGCA	4860
GGGACAGTTA	TTCTTCTGAT	AGACATTTAT	CACAATACCA	TGATCATCAC	AAAGACAGGC	4920
ATCAGGGAGA	TGCTTACAAG	AAAAGTGA	CTCAGGAAAAG	GCCATATTCA	GCCTTCAGTA	4980
ATGGAAAAGA	TCACAGAGAC	TGGGATCACT	ACAAACAGGA	CAGCAGATAC	TACAGTGATA	5040
GTAAACATAG	AAAGTTAGAT	GACCACAGGA	GCAGAGACCA	CAGGTCAAAC	CTGGAAGGAA	5100
ACTTAAAAGA	CAGCCGGGGT	CATTCAGATC	ACCGCTCCCA	TTCAGACCAC	AGGATACACT	5160
CAGATCACCG	TTCCACTTCA	GAATACAGCC	ATCATAAATC	TTCGAGAGAT	TATAGATACC	5220
ACTCAGACTG	GCAAATGGAC	CACAGAGCTT	CTGGTAGTGG	CCCGAGGTCA	CCACTAGATC	5280
AGAGGTCTCC	TTATGGTTCA	AGATCTCCCC	TAGGACACAG	ATCTCCATTT	GAACACTCAT	5340
CAGATCACAA	AAGTACACCT	GAACATACAT	GGAGTAGCCG	GAAGACATAA	CAAAGACTGA	5400
CATTTTCTGG	ACCTTCTTTT	TAGCCATATA	CAGTAAACTA	ACACAGTAAT	TGCCTTACAT	5460
GACTTGAAAG	ATATGGACTG	GATATTCTAT	CAGTAGCAGT	ATTGTTACTT	CTTTCAGGA	5520

TGCAAGGTCT	ATTATCCCAA	CAGAAGAAAA	ATATTTTGT	ATTTAAAGTT	TATGCTGCAC	5580
TGTGCTGCAA	ATGTTGTGGC	ACTTTTTTTT	TAAGAAATGG	AAGATGTTTA	CTTTTACAGG	5640
GACCTCAACA	CTGCCCCTTT	CAGACTGGAT	CTTACTATAA	AACTCTTCAT	GTCAAAGTGG	5700
TTCTAGGCTG	AACACAGATT	AAATTATGTT	TGTAAATGAA	CACTTAAACA	CTGACCTGTG	5760
CTTATGTTTC	AGGAAAGAAT	GGGGGATTTA	TTTTGTTTTA	TTTCTTGGTA	GAGAACTCTC	5820
AAGGACTTTG	TTCACCTTCC	AAAGCTACTT	GTTTACATTG	TACACTGCGA	CCACCTTGCC	5880
GCTTTTCATC	ACAAGCTTGA	ATATTTAAAT	TCTGTACCTA	CAGTTGTAAA	ATAGCCAGGA	5940
TTTCTCCTGT	TTGTGATCAG	TTATAATGCC	TTTTTATGAA	ACAAACAAAC	AAACAAAAAA	6000
CAATTAAAAA	AAAAAACACA	ACAAAACCAA	CAAATGGCTG	TAAATTATTG	TAAATTAATT	6060
AAATGAGCTT	TTTTCCGTCA	GGCTTTTTTT	GGCTGTTCCCT	TTCCCCAACA	ACTCAGGCCT	6120
TCTTTTCACA	AAGTCAGTAT	ACTTACATGT	TTTAATAAAA	TATCTCGATG	GAATCAGAAT	6180
GTAAAAATGG	GGAAGGGAAT	ATTTTATTCC	ATTAGTGCT	CCTTTTTTAT	TGGATACTTT	6240
TACATACCTG	TTTTTGTTTG	TTTTATTTTA	TTTTTTTTTT	CTATTAAACT	GTCAGTGTTG	6300
TGATTGTTGT	AATGAACAGT	GAGAATATCC	CACTCTAAAC	TGTGCCCTGG	AAAGCTTTTC	6360
AGGTGCATTG	GTTTAAAAGA	AGGAAGTGTT	CTATAGGTGA	ACACTTCAAA	ACCCAGATCA	6420
GCCAAGATTC	ATTGTAAATC	CATTTGTTTT	CCCTCTTTAA	CATGGGCAAT	AATGTCAAAT	6480
GTGCTATGCA	GCAGTTAATA	TTTTAGAAGA	TTTGAATGAC	TTTATTAACA	GAATTGTTAC	6540
AATGCACACT	GATTGTACAT	AGATAACTTC	TATCTGACAA	ATTAAATTAA	CTAAAACCAA	6600
AAAAAACC						6608

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp	Glu	Ile	Val	Ser	Val	Lys	His	Leu	His	Lys	Lys	Ile	Lys	Thr	Glu
1					5					10					15
Lys	Glu	Asn	Glu	Glu	Lys	Pro	Glu	Pro	Asp	Ile	Gly	Ile	Lys	Lys	Glu
					20					25					30
Ala	Glu	Glu	Lys	Arg	Glu	Thr	Lys	Glu	Lys	Glu	Asn	Lys	Arg	Glu	Leu
					35					40					45
Lys	Arg	Glu	Lys	Lys	Glu	Lys	Glu	Asp	Lys	Lys	Glu	Leu	Lys	Glu	Lys
					50					55					60
Asp	Asn	Lys	Glu	Lys	Arg	Glu	Asn	Lys	Val	Lys	Glu	Ser	Thr	Gln	Lys
					65					70					75
															80
Glu	Lys	Glu	Val	Lys	Glu	Glu	Lys								
															85

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GATGAGATTG TTTCAGTGAA ACATCTACAT AAAAAAATAA AAACAGAAAA AAGAAAATGA

AGAAAAGCCT GAGCCAGATA TTGGTATAAA GAAGGAAGCT GAAGAAAAAA GAGAGACAAA	120
AGAGAAGGAA AATAAAAGGG AATTGAAAAG GGAGAAAAAA GAAAAAGAGG ATAAGAAAGA	180
ATTAAAAGAA AAAGATAATA AAGAAAAGAG AGAAAACAAA GTAAAAGAAT CCACACAGAA	240
AGAAAAGGAA GTGAAGGAAG AGAAG	265

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GATGGGATTG TTTCAGTGAA ACATCCACAT AAAAAAATAA AAGCAGAAAA AAGAAAATGA	60
AGAAAAGAT GAGCCAGAGA TTGGTATAAA GAAGGAAGCT GGAGAAAAAA GAGAGACAAA	120
AGAAAAGGAA AATAAGA	137

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

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Asp Gly Ile Val Ser Val Lys His Pro His Lys Lys Ile Lys Ala Glu
1 5 10 15
Lys Glu Asn Glu Glu Lys Asp Glu Pro Glu Ile Gly Ile Lys Lys Glu
 20 25 30
Ala Gly Glu Lys Arg Glu Thr Lys Glu Lys Glu Asn Lys
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ATTTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA	60
AAGATGGTGT TAGATCATTT AGTGATTCAG AGAATGGACA CCACAGGGAA AACTGTACTA	120
CATACAGGCT CTACTCCTTC AAGCTCAACA CCTTTTAATA AGGAAGAGTT ATCAGCAATT	180
TTGAAGTTTG GTGCTGAGGA ACTTTTAAA GAACCTGAAN NNGAAGAAGA GGAGCCTCAG	240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAACTC GAGAAAATGA GTCAGGCCCA	300
TTAACTGTAG GAGATGAGTT ACTTTCACAG TTCAAGGTAG CTAACCTTTC CAATATGGAT	360
GAAGATGACA TTGAATTGGA ACCAGAACAA AATCTAAGAA ACTGGGAAGA AATCATTCOA	420
GAAGTTCAGT GGCGACGAAT AGAGGGGNG GAAAGACAAA AAGAACTTGA AGAAATATAT	480
ATGCTTCCAA GAATGAGAAA CTGTGCAAAA CAGATCAGCT TTAATGGAAA TGAAGGGAGA	540

TGCAGTAGGA GCAGAAGATA TTCTGGATCT GATAGTGATT CCATCTCAGA AAGAAAACGA	600
CCAAAAAAC GTGGACGACC ACGAACTATT CCCCCTGAAA ACATTAAAGG ATTTAGTGAT	660
GCAGAGATTA GACGATTTAT CAAGAGTTAC AAGAAATTTG GTGGCCCAGT TGAAAGGTTA	720
GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAATCTG AAACAGACCT TAGACGTCTG	780
GGAGAACTTG TACATAATGG ATGCATTAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA	840
AGAACAGGTG GTAGATTTGG GAAAGTTAAA GGCCCAACAT TCCGAATAGC AGGAGTGCAG	900
GTGAATGCAA AGCTAGTCAT TTCTCACGAA GAAGAGTTGG CACCATTGCA TAAATCGATT	960
CCTTCAGATC CAGAAGAAAG GAAAAGATAT GTCATCCCAT ACCACACCAA AGCAGCTCAT	1020
TTTGATATAG ATTGGGGTAA AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT	1080
GGTTATGGCA GTTGGGAAAT GATAAAAATG GATCCTGATC TCAGTTTGAC ACAGAAGATT	1140
TTACCTGATG ATCCAGATAA GAAACCCAG GCTAAGCAGT TACAGACTCG TGCAGATTAC	1200
CTCATTAAT TACTGAATAA AGACCTTGCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA	1260
GGCAATTCAA AGAGGAGAAA AACAAGAAGT AAGAAGAATA AAGCAACAAA GGCTGC	1316

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Asp Ala Arg Arg Tyr Leu Gly Lys Asn Leu Gly His Leu Arg Ile Ala

1

5

10

15

Ser Gln Thr His Tyr Phe Glu Asn Ile Arg Ser Thr Arg Lys Gly Ile

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				20					25					30		
Leu	Asp	Leu	His	Leu	Val	Thr	Val	Asp	Phe	Leu	Phe	Asn	Phe	Leu	Ile	
		35						40				45				
Leu	Thr	Met	Asn	Gly	His	Ser	Asp	Glu	Glu	Ser	Val	Arg	Asn	Ser	Ser	
		50					55					60				
Gly	Glu	Ser	Ser	Arg	Ser	Asp	Asp	Asp	Ser	Ala	Gly	Ser	Ala	Ser	Gly	
65					70						75				80	
Ser	Gly	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Asp	Gly	Ser	Ser	Ser	
				85					90					95		
Gln	Ser	Gly	Ser	Ser	Asp	Ser	Glu	Ser	Gly	Ser	Glu	Ser	Gly	Ser	Gln	
			100					105					110			
Ser	Glu	Ser	Glu	Ser	Asp	Thr	Ser	Arg	Glu	Lys	Lys	Gln	Val	Gln	Ala	
		115					120					125				
Lys	Pro	Pro	Lys	Ala	Asp	Gly	Ser	Glu	Phe	Trp	Lys	Ser	Ser	Pro	Ser	
		130				135					140					
Ile	Leu	Ala	Val	Gln	Arg	Ser	Ala	Val	Leu	Lys	Lys	Gln	Gln	Gln	Gln	
145					150						155				160	
Gln	Lys	Ala	Ala	Ser	Ser	Asp	Ser	Gly	Ser	Glu	Glu	Asp	Ser	Ser	Ser	
				165					170					175		
Ser	Glu	Asp	Ser	Ala	Asp	Asp	Ser	Ser	Ser	Glu	Thr	Lys	Lys	Lys	Lys	
			180					185					190			
His	Lys	Asp	Glu	Asp	Trp	Gln	Met	Ser	Gly	Ser	Gly	Ser	Val	Ser	Gly	
		195					200					205				
Thr	Gly	Ser	Asp	Ser	Glu	Ser	Ala	Glu	Asp	Gly	Asp	Lys	Ser	Ser	Cys	
		210					215					220				

Glu Glu Ser Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg
225 230 235 240
Lys Pro Pro Ser Arg Ile Lys Pro Lys Ser Gly Lys Lys Ser Thr Gly
245 250 255
Gln Lys Lys Arg Gln Leu Asp Ser Ser Glu Glu Glu Glu Asp Asp Asp
260 265 270
Glu Asp Tyr Asp Lys Arg Gly Ser Arg Arg Gln Ala Thr Val Asn Val
275 280 285
Ser Tyr Lys Glu Ala Glu Glu Thr Lys Thr Asp Ser Asp Asp Leu Leu
290 295 300
Glu Val Cys Gly Glu Asp Val Pro Gln Thr Glu Glu Asp Glu Phe Glu
305 310 315 320
Thr Ile Glu Lys Phe Met Asp Ser Arg Ile Gly Arg Lys Gly Ala Thr
325 330 335
Gly Ala Ser Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn
340 345 350
Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile
355 360 365
Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu
370 375 380
Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr
385 390 395 400
Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro
405 410 415
Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu

420	425	430
His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln		
435	440	445
Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu		
450	455	460
Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys		
465	470	475
Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr		
485	490	495
Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val		
500	505	510
Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu		
515	520	525
Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp		
530	535	540
Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys		
545	550	555
Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln		
565	570	575
Leu Tyr Gly Pro Phe Leu Leu Arg Val Pro Leu Ser Thr Leu Thr Ser		
580	585	590
Trp Gln Arg Glu Ile Gln Thr Trp Ala Pro Gln Met Asn Ala Val Val		
595	600	605
Tyr Leu Gly Asp Ile Thr Ser Arg Asn Met Ile Arg Thr His Glu Trp		
610	615	620

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Met	His	Pro	Gln	Thr	Lys	Arg	Leu	Lys	Phe	Asn	Ile	Leu	Leu	Thr	Thr
625					630					635					640
Tyr	Glu	Ile	Leu	Leu	Lys	Asp	Lys	Ser	Phe	Leu	Gly	Gly	Leu	Asn	Trp
				645					650					655	
Ala	Phe	Ile	Gly	Val	Asp	Glu	Ala	His	Arg	Leu	Lys	Asn	Asp	Asp	Ser
			660					665					670		
Leu	Leu	Tyr	Arg	Thr	Leu	Ile	Asp	Phe	Lys	Ser	Asn	His	Arg	Leu	Leu
		675					680					685			
Ile	Thr	Gly	Thr	Pro	Leu	Gln	Asn	Ser	Leu	Lys	Glu	Leu	Trp	Ser	Leu
	690					695					700				
Leu	His	Phe	Ile	Met	Pro	Glu	Lys	Phe	Ser	Ser	Trp	Glu	Asp	Phe	Glu
705					710					715					720
Glu	Glu	His	Gly	Lys	Gly	Arg	Glu	Tyr	Gly	Tyr	Ala	Ser	Leu	His	Lys
				725					730				735		
Glu	Leu	Glu	Pro	Phe	Leu	Leu	Arg	Arg	Val	Lys	Lys	Asp	Val	Glu	Lys
			740					745					750		
Ser	Leu	Pro	Ala	Lys	Val	Glu	Gln	Ile	Leu	Arg	Met	Glu	Met	Ser	Ala
		755					760					765			
Leu	Gln	Lys	Gln	Tyr	Tyr	Lys	Trp	Ile	Leu	Thr	Arg	Asn	Tyr	Lys	Ala
	770					775					780				
Leu	Ser	Lys	Gly	Ser	Lys	Gly	Ser	Thr	Ser	Gly	Phe	Leu	Asn	Ile	Met
785					790					795					800
Met	Glu	Leu	Lys	Lys	Cys	Cys	Asn	His	Cys	Tyr	Leu	Ile	Lys	Pro	Pro
				805					810				815		
Asp	Asp	Asn	Glu	Phe	Tyr	Asn	Lys	Gln	Glu	Ala	Leu	Gln	His	Leu	Ile

820	825	830
Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu		
835	840	845
Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met		
850	855	860
Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln		
865	870	875
Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp		
885	890	895
His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr		
900	905	910
Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val		
915	920	925
Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala		
930	935	940
Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu		
945	950	955
Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys		
965	970	975
Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly		
980	985	990
Lys Thr Val Leu His Thr Gly Ser Ala Pro Ser Ser Ser Thr Pro Phe		
995	1000	1005
Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu		
1010	1015	1020

Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile
1025 1030 1035 1040
Asp Glu Ile Leu Lys Arg Ala Glu Thr His Glu Asn Glu Pro Gly Pro
1045 1050 1055
Leu Ser Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn Phe
1060 1065 1070
Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg Asn Ser
1075 1080 1085
Lys Asn Trp Glu Glu Ile Ile Pro Glu Glu Gln Arg Arg Arg Leu Glu
1090 1095 1100
Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr Met Leu Pro Arg
1105 1110 1115 1120
Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly Ser Glu Gly Arg
1125 1130 1135
Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser Asp Ser Ile Ser
1140 1145 1150
Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg
1155 1160 1165
Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys
1170 1175 1180
Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Ile Ala
1185 1190 1195 1200
Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu
1205 1210 1215
Gly Glu Leu Val His Asn Gly Cys Val Lys Ala Leu Lys Asp Ser Ser

1220	1225	1230
Ser Gly Thr Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro		
1235	1240	1245
Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ala		
1250	1255	1260
His Glu Asp Glu Leu Ile Pro Leu His Lys Ser Ile Pro Ser Asp Pro		
1265	1270	1275
Glu Glu Arg Lys Gln Tyr Thr Ile Pro Cys His Thr Lys Ala Ala His		
1285	1290	1295
Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Ile Gly		
1300	1305	1310
Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro		
1315	1320	1325
Asp Leu Ser Leu Thr His Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys		
1330	1335	1340
Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile Lys Leu		
1345	1350	1355
Leu Ser Arg Asp Leu Ala Lys Arg Glu Ala Gln Arg Leu Cys Gly Ala		
1365	1370	1375
Gly Gly Ser Lys Arg Arg Lys Thr Arg Ala Lys Lys Ser Lys Ala Met		
1380	1385	1390
Lys Ser Ile Lys Val Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro Leu		
1395	1400	1405
Pro Ser Glu Lys Ser Asp Glu Asp Asp Asp Lys Leu Asn Asp Ser Lys		
1410	1415	1420

Pro Glu Ser Lys Asp Arg Ser Lys Lys Ser Val Val Ser Asp Ala Pro
1425 1430 1435 1440
Val His Ile Thr Ala Ser Gly Glu Pro Val Pro Ile Ala Glu Glu Ser
1445 1450 1455
Glu Glu Leu Asp Gln Lys Thr Phe Ser Ile Cys Lys Glu Arg Met Arg
1460 1465 1470
Pro Val Lys Ala Ala Leu Lys Gln Leu Asp Arg Pro Glu Lys Gly Leu
1475 1480 1485
Ser Glu Arg Glu Gln Leu Glu His Thr Arg Gln Cys Leu Ile Lys Ile
1490 1495 1500
Gly Asp His Ile Thr Glu Cys Leu Lys Glu Tyr Ser Asn Pro Glu Gln
1505 1510 1515 1520
Ile Lys Gln Trp Arg Lys Asn Leu Trp Ile Phe Val Ser Lys Phe Thr
1525 1530 1535
Glu Phe Asp Ala Arg Lys Leu His Lys Leu Tyr Lys His Ala Ile Lys
1540 1545 1550
Lys Arg Gln Glu Ser Gln Gln Asn Ser Asp Gln Asn Ser Asn Val Ala
1555 1560 1565
Thr Thr His Val Ile Arg Asn Pro Asp Met Glu Arg Leu Lys Glu Asn
1570 1575 1580
Thr Asn His Asp Asp Ser Ser Arg Asp Ser Tyr Ser Ser Asp Arg His
1585 1590 1595 1600
Leu Ser Gln Tyr His Asp His His Lys Asp Arg His Gln Gly Asp Ser
1605 1610 1615
Tyr Lys Lys Ser Asp Ser Arg Lys Arg Pro Tyr Ser Ser Phe Ser Asn

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1620	1625	1630
Gly Lys Asp His Arg Glu Trp Asp His Tyr Arg Gln Asp Ser Arg Tyr		
1635	1640	1645
Tyr Ser Asp Arg Glu Lys His Arg Lys Leu Asp Asp His Arg Ser Arg		
1650	1655	1660
Glu His Arg Pro Ser Leu Glu Gly Gly Leu Lys Asp Leu Asp Gln Arg		
1665	1670	1675
Ser Pro Tyr Gly Ser Arg Ser Pro Phe Glu His Ser Ala Glu His Arg		1680
1685	1690	1695
Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Lys Leu		
1700	1705	1710
Met Ser Leu Ser Ser Gly Thr Leu Phe Xaa Pro Leu Thr Xaa Leu Glu		
1715	1720	1725
Arg Tyr Gly Leu Asp Ile Leu Ser Val Ala Val Leu Leu Leu Leu Ser		
1730	1735	1740
Arg Met Gln Gly Leu Leu Ser Gln Gln Lys Lys Asn Ile Phe Val Phe		
1745	1750	1755
Lys Val Tyr Ala Ala Leu Cys Cys Lys Cys Cys Gly Thr Phe Phe Leu		1760
1765	1770	1775
Arg Asn Gly Arg Cys Leu Leu Leu Gln Gly Pro Gln His Cys Pro Phe		
1780	1785	1790
Gln Thr Gly Ser Tyr Tyr Lys Thr Leu His Val Lys Val Val Leu Gly		
1795	1800	1805
Xaa Thr Gln Ile Lys Leu Cys Leu Xaa Met Asn Thr Xaa Thr Leu Thr		
1810	1815	1820

Cys Ala Tyr Val Ser Gly Lys Asn Gly Gly Phe Ile Leu Phe Tyr Phe			
1825	1830	1835	1840
Leu Val Glu Asn Ser Gln Gly Leu Cys Ser Leu Ser Lys Ala Thr Cys			
	1845	1850	1855
Leu His Cys Thr Leu Arg Pro Pro Cys Arg Phe Ser Ser Gln Ala Xaa			
	1860	1865	1870
Ile Phe Lys Phe Cys Thr Tyr Ser Cys Lys Ile Ala Arg Ile Ser Pro			
	1875	1880	1885
Val Cys Asp Gln Leu Xaa Cys Leu Phe Met Lys Gln Thr Asn Lys Gln			
	1890	1895	1900
Lys Thr Ile Lys Lys Lys Asn Thr Thr Lys Pro Thr Asn Gly Cys Lys			
1905	1910	1915	1920
Leu Leu Xaa Ile Asn Xaa Met Ser Phe Phe Pro Ser Gly Phe Phe Trp			
	1925	1930	1935
Leu Phe Leu Ser Pro Thr Thr Gln Ala Phe Phe Ser Gln Ser Gln Tyr			
	1940	1945	1950
Thr Tyr Met Phe Xaa Xaa Asn Ile Ser Met Glu Ser Glu Cys Lys Asn			
	1955	1960	1965
Gly Glu Gly Asn Ile Leu Phe His Leu Val Leu Leu Phe Tyr Trp Ile			
	1970	1975	1980
Leu Leu His Thr Cys Phe Trp Leu Phe Tyr Phe Ile Phe Phe Phe Tyr			
1985	1990	1995	2000
Xaa Thr Val Ser Val Val Ile Val Val Met Asn Ser Glu Asn Ile Pro			
	2005	2010	2015
Leu Xaa Thr Val Pro Trp Lys Ala Phe Gln Val His Trp Phe Lys Arg			

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2020	2025	2030	
Arg Lys Cys Ser Ile Gly Glu His Phe Lys Thr Gln Ile Ser Gln Asp			
2035	2040	2045	
Ser Leu Xaa Ile His Leu Phe Ser Leu Phe Asn Met Gly Asn Asn Val			
2050	2055	2060	
Lys Cys Ala Met Gln Gln Leu Ile Phe Xaa Lys Ile Xaa Met Thr Leu			
2065	2070	2075	2080
Leu Thr Glu Leu Leu Gln Cys Thr Leu Ile Val His Arg Xaa Leu Leu			
2085	2090	2095	
Ser Asp Lys Leu Asn Xaa Leu Lys Pro Lys Lys Thr			
2100	2105		

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Phe Ala Leu Cys Pro Pro Val Thr Gln Arg Glu Pro Gln Glu Thr Arg			
1	5	10	15
Glu Cys Arg Lys Phe Ile Phe Glu Ile Leu Ile Phe Glu Glu Ile Cys			
20	25	30	
Ile His Thr His Leu Leu Leu Ile Gly Asp Phe Cys Phe Ile Asn Phe			

35	40	45
Leu Ile Phe Thr Met Asn Gly His Ser Asp Glu Glu Ser Val Arg Asn		
50	55	60
Gly Ser Gly Glu Ser Ser Gln Ser Gly Asp Asp Cys Gly Ser Ala Ser		
65	70	75
Gly Ser Gly Ser Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser		
85	90	95
Ser Gln Ser Gly Ser Ser Asp Ser Asp Ser Gly Ser Asp Ser Gly Ser		
100	105	110
Gln Ser Glu Ser Glu Ser Asp Thr Ser Arg Glu Asn Lys Val Gln Ala		
115	120	125
Lys Pro Pro Lys Val Asp Gly Ala Glu Phe Trp Lys Ser Ser Pro Ser		
130	135	140
Ile Leu Ala Val Gln Arg Ser Ala Met Leu Arg Lys Gln Pro Gln Gln		
145	150	155
Ala Gln Gln Gln Arg Pro Ala Ser Ser Asn Ser Gly Ser Glu Glu Asp		
165	170	175
Ser Ser Ser Ser Glu Asp Ser Asp Asp Ser Ser Ser Gly Ala Lys Arg		
180	185	190
Lys Lys His Asn Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Pro		
195	200	205
Ser Gln Leu Gly Ser Asp Ser Glu Ser Glu Glu Glu Arg Asp Lys Ser		
210	215	220
Ser Cys Asp Gly Thr Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Arg		
225	230	235
		240

Ser	Arg	Lys	Pro	Gln	Asn	Arg	Ser	Lys	Ser	Lys	Asn	Gly	Lys	Lys	Ile
				245					250					255	
Leu	Gly	Gln	Lys	Lys	Arg	Gln	Ile	Asp	Ser	Ser	Glu	Asp	Glu	Asp	Asp
				260					265					270	
Glu	Asp	Tyr	Asp	Asn	Asp	Lys	Arg	Ser	Ser	Arg	Arg	Gln	Ala	Thr	Val
				275					280					285	
Asn	Val	Ser	Tyr	Lys	Glu	Asp	Glu	Glu	Met	Lys	Thr	Asp	Ser	Asp	Asp
				290					295					300	
Leu	Leu	Glu	Val	Cys	Gly	Glu	Asp	Val	Pro	Gln	Pro	Glu	Asp	Glu	Glu
305					310					315				320	
Phe	Glu	Thr	Ile	Glu	Arg	Val	Met	Asp	Cys	Arg	Val	Gly	Arg	Lys	Gly
				325					330					335	
Ala	Thr	Gly	Ala	Thr	Thr	Thr	Ile	Tyr	Ala	Val	Glu	Ala	Asp	Gly	Asp
				340					345					350	
Pro	Asn	Ala	Gly	Phe	Glu	Arg	Asn	Lys	Glu	Pro	Gly	Asp	Ile	Gln	Tyr
				355					360					365	
Leu	Ile	Lys	Trp	Lys	Gly	Trp	Ser	His	Ile	His	Asn	Thr	Trp	Glu	Thr
				370					375					380	
Glu	Glu	Thr	Leu	Lys	Gln	Gln	Asn	Val	Arg	Gly	Met	Lys	Lys	Leu	Asp
385					390					395				400	
Asn	Tyr	Lys	Lys	Lys	Asp	Gln	Glu	Thr	Lys	Arg	Trp	Leu	Lys	Asn	Ala
				405					410					415	
Ser	Pro	Glu	Asp	Val	Glu	Tyr	Tyr	Asn	Cys	Gln	Gln	Glu	Leu	Thr	Asp
				420					425					430	
Asp	Leu	His	Lys	Gln	Tyr	Gln	Ile	Val	Glu	Arg	Ile	Ile	Ala	His	Ser

435	440	445	
Asn Gln Lys Ser Ala Ala Gly Leu Pro Asp Tyr Tyr Cys Lys Trp Gln			
450	455	460	
Gly Leu Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ser			
465	470	475	480
Lys Lys Phe Gln Thr Cys Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser			
	485	490	495
Lys Thr Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg			
	500	505	510
Phe Val Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Gly			
	515	520	525
Leu Glu Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His			
	530	535	540
Ser Trp Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu			
545	550	555	560
Gly Lys Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu			
	565	570	575
His Gln Leu Tyr Gly Pro Phe Leu Leu Val Val Pro Leu Ser Thr Leu			
	580	585	590
Thr Ser Trp Gln Arg Glu Ile Gln Thr Trp Ala Ser Gln Met Asn Ala			
	595	600	605
Val Val Tyr Leu Gly Asp Ile Asn Ser Arg Asn Met Ile Arg Thr His			
	610	615	620
Glu Trp Met His Pro Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu			
625	630	635	640

Thr	Thr	Tyr	Glu	Ile	Leu	Leu	Lys	Asp	Lys	Ala	Phe	Leu	Gly	Gly	Leu
645				650				655							
Asn	Trp	Ala	Phe	Ile	Gly	Val	Asp	Glu	Ala	His	Arg	Leu	Lys	Asn	Asp
660				665				670							
Asp	Ser	Leu	Leu	Tyr	Lys	Thr	Leu	Ile	Asp	Phe	Lys	Ser	Asn	His	Arg
675				680				685							
Leu	Leu	Ile	Thr	Gly	Thr	Pro	Leu	Gln	Asn	Ser	Leu	Lys	Glu	Leu	Trp
690				695				700							
Ser	Leu	Leu	His	Phe	Ile	Met	Pro	Glu	Lys	Phe	Ser	Ser	Trp	Glu	Asp
705	710				715				720						
Phe	Glu	Glu	Glu	His	Gly	Lys	Gly	Arg	Glu	Tyr	Gly	Tyr	Ala	Ser	Leu
725				730				735							
His	Lys	Glu	Leu	Glu	Pro	Phe	Leu	Leu	Arg	Arg	Val	Lys	Lys	Asp	Val
740				745				750							
Glu	Lys	Ser	Leu	Pro	Ala	Lys	Val	Glu	Gln	Ile	Leu	Arg	Met	Glu	Met
755				760				765							
Ser	Ala	Leu	Gln	Lys	Gln	Tyr	Tyr	Lys	Trp	Ile	Leu	Thr	Arg	Asn	Tyr
770				775				780							
Lys	Ala	Leu	Ser	Lys	Gly	Ser	Lys	Gly	Ser	Thr	Ser	Gly	Phe	Leu	Asn
785	790				795				800						
Ile	Met	Met	Glu	Leu	Lys	Lys	Cys	Cys	Asn	His	Cys	Tyr	Leu	Ile	Lys
805				810				815							
Pro	Pro	Asp	Asn	Asn	Glu	Phe	Tyr	Asn	Lys	Gln	Glu	Ala	Leu	Gln	His
820				825				830							
Leu	Ile	Arg	Ser	Ser	Gly	Lys	Leu	Ile	Leu	Leu	Asp	Lys	Leu	Leu	Ile

835	840	845	
Arg Leu Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val			
850	855	860	
Arg Met Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro			
865	870	875	880
Phe Gln Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala			
885	890	895	
Leu Asp His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu			
900	905	910	
Ser Thr Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr			
915	920	925	
Val Val Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala			
930	935	940	
Gln Ala Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr			
945	950	955	960
Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala			
965	970	975	
Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr			
980	985	990	
Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser Ser Thr			
995	1000	1005	
Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu			
1010	1015	1020	
Glu Leu Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met			
1025	1030	1035	1040

Asp	Ile	Asp	Glu	Ile	Leu	Lys	Arg	Ala	Glu	Thr	Arg	Glu	Asn	Glu	Pro	
1045					1050					1055						
Gly	Pro	Leu	Thr	Val	Gly	Asp	Glu	Leu	Leu	Ser	Gln	Phe	Lys	Val	Ala	
1060					1065					1070						
Asn	Phe	Ser	Asn	Met	Asp	Glu	Asp	Asp	Ile	Glu	Leu	Glu	Pro	Glu	Arg	
1075					1080					1085						
Asn	Ser	Arg	Asn	Trp	Glu	Glu	Ile	Ile	Pro	Glu	Ser	Gln	Arg	Arg	Arg	
1090					1095					1100						
Ile	Glu	Glu	Glu	Glu	Arg	Gln	Lys	Glu	Leu	Glu	Glu	Ile	Tyr	Met	Leu	
1105					1110					1115					1120	
Pro	Arg	Met	Arg	Asn	Cys	Ala	Lys	Gln	Ile	Ser	Phe	Asn	Gly	Ser	Glu	
1125					1130					1135						
Gly	Arg	Arg	Ser	Arg	Ser	Arg	Arg	Tyr	Ser	Gly	Ser	Asp	Ser	Asp	Ser	
1140					1145					1150						
Ile	Thr	Glu	Arg	Lys	Arg	Pro	Lys	Lys	Arg	Gly	Arg	Pro	Arg	Thr	Ile	
1155					1160					1165						
Pro	Arg	Glu	Asn	Ile	Lys	Gly	Phe	Ser	Asp	Ala	Glu	Ile	Arg	Arg	Phe	
1170					1175					1180						
Ile	Lys	Ser	Tyr	Lys	Lys	Phe	Gly	Gly	Pro	Leu	Glu	Arg	Leu	Asp	Ala	
1185					1190					1195					1200	
Val	Ala	Arg	Asp	Ala	Glu	Leu	Val	Asp	Lys	Ser	Glu	Thr	Asp	Leu	Arg	
1205					1210					1215						
Arg	Leu	Gly	Glu	Leu	Val	His	Asn	Gly	Cys	Ile	Lys	Ala	Leu	Lys	Asp	
1220					1225					1230						
Asn	Ser	Ser	Gly	Gln	Glu	Arg	Ala	Gly	Gly	Arg	Leu	Gly	Lys	Val	Lys	

1235	1240	1245	
Gly Pro Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val			
1250	1255	1260	
Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser			
1265	1270	1275	1280
Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala			
1285	1290	1295	
Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu			
1300	1305	1310	
Val Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met			
1315	1320	1325	
Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp			
1330	1335	1340	
Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr Leu Ile			
1345	1350	1355	1360
Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg Leu Ala			
1365	1370	1375	
Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Asn Lys Lys Asn Lys			
1380	1385	1390	
Met Lys Ala Ser Lys Ile Lys Glu Glu Ile Lys Ser Asp Ser Ser Pro			
1395	1400	1405	
Gln Pro Ser Glu Lys Ser Asp Glu Asp Asp Glu Glu Glu Asp Asn Lys			
1410	1415	1420	
Val Asn Glu Met Lys Ser Glu Asn Lys Glu Lys Ser Lys Lys Ile Pro			
1425	1430	1435	1440

Leu	Leu	Asp	Thr	Pro	Val	His	Ile	Thr	Ala	Thr	Ser	Glu	Pro	Val	Pro
				1445					1450					1455	
Ile	Ser	Glu	Glu	Ser	Glu	Glu	Leu	His	Gln	Lys	Thr	Phe	Ser	Val	Cys
				1460					1465					1470	
Lys	Glu	Arg	Met	Arg	Pro	Val	Lys	Ala	Ala	Leu	Lys	Gln	Leu	Asp	Arg
				1475					1480					1485	
Pro	Glu	Lys	Gly	Leu	Ser	Glu	Arg	Glu	Gln	Leu	Glu	His	Thr	Arg	Gln
				1490					1495					1500	
Cys	Leu	Ile	Lys	Ile	Gly	Asp	His	Ile	Thr	Glu	Cys	Leu	Lys	Glu	Tyr
1505					1510					1515					1520
Thr	Asn	Pro	Glu	Gln	Ile	Lys	Gln	Trp	Arg	Lys	Asn	Leu	Trp	Ile	Phe
				1525						1530					1535
Val	Ser	Lys	Phe	Thr	Glu	Phe	Asp	Ala	Arg	Lys	Leu	His	Lys	Leu	Tyr
				1540					1545					1550	
Lys	His	Ala	Ile	Lys	Lys	Arg	Gln	Glu	Ser	Gln	Gln	His	Asn	Asp	Gln
				1555					1560					1565	
Asn	Ile	Ser	Ser	Asn	Val	Asn	Thr	His	Val	Ile	Arg	Asn	Pro	Asp	Val
				1570					1575					1580	
Glu	Arg	Leu	Lys	Glu	Thr	Thr	Asn	His	Asp	Asp	Ser	Ser	Arg	Asp	Ser
1585					1590					1595					1600
Tyr	Ser	Ser	Asp	Arg	His	Leu	Ser	Gln	Tyr	His	Asp	His	His	Lys	Asp
				1605						1610					1615
Arg	His	Gln	Gly	Asp	Ala	Tyr	Lys	Lys	Ser	Asp	Ser	Arg	Lys	Arg	Pro
				1620						1625				1630	
Tyr	Ser	Ala	Phe	Ser	Asn	Gly	Lys	Asp	His	Arg	Asp	Trp	Asp	His	Tyr

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1635	1640	1645	
Lys Gln Asp Ser Arg Tyr Tyr Ser Asp Ser Lys His Arg Lys Leu Asp			
1650	1655	1660	
Asp His Arg Ser Arg Asp His Arg Ser Asn Leu Glu Gly Asn Leu Lys			
1665	1670	1675	1680
Asp Ser Arg Gly His Ser Asp His Arg Ser His Ser Asp His Arg Ile			
	1685	1690	1695
His Ser Asp His Arg Ser Thr Ser Glu Tyr Ser His His Lys Ser Ser			
	1700	1705	1710
Arg Asp Tyr Arg Tyr His Ser Asp Trp Gln Met Asp His Arg Ala Ser			
	1715	1720	1725
Gly Ser Gly Pro Arg Ser Pro Leu Asp Gln Arg Ser Pro Tyr Gly Ser			
	1730	1735	1740
Arg Ser Pro Leu Gly His Arg Ser Pro Phe Glu His Ser Ser Asp His			
1745	1750	1755	1760
Lys Ser Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr Xaa Gln Arg			
	1765	1770	1775
Leu Thr Phe Ser Gly Pro Ser Phe Xaa Pro Tyr Thr Val Asn Xaa His			
	1780	1785	1790
Ser Asn Cys			
1795			

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Lys	Thr	Xaa	Glu	Pro	Gly	Glu	Ile	Gln	Tyr	Leu	Ile	Lys	Trp	Lys	Gly
1				5					10					15	
Trp	Ser	His	Ile	His	Asn	Thr	Trp	Glu	Thr	Glu	Glu	Thr	Leu	Lys	Gln
				20					25					30	
Gln	Asn	Val	Arg	Gly	Met	Lys	Lys	Leu	Asp	Asn	Tyr	Lys	Lys	Lys	Asp
				35					40					45	
Gln	Glu	Thr	Lys	Arg	Trp	Leu	Lys	Asn	Ala	Ser	Pro	Glu	Asp	Val	Glu
				50					55					60	
Tyr	Tyr	Asn	Cys	Gln	Gln	Glu	Leu	Thr	Asp	Asp	Leu	His	Lys	Gln	Tyr
				65					70					75	
Gln	Ile	Val	Glu	Arg	Thr	Asn	Xaa	Ser	Phe	Gln	Ser	Lys	Ser	Ala	Ala
				85					90					95	
Gly	Tyr	Pro													

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Ile Tyr Arg Leu Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu

1 5 10 15

Arg Ala Lys Lys Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met
20 25 30

Asp Thr Thr Gly Lys Thr Val Leu His Thr Gly Ser Thr Pro Ser Ser
35 40 45

Ser Thr Pro Phe Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly

50 55 60

Ala Glu Glu Leu Phe Lys Glu Pro Glu Xaa Glu Glu Glu Glu Pro Gln
65 70 75 80

Glu Met Asp Ile Asp Glu Ile Leu Lys Arg Xaa Glu Thr Arg Glu Asn
85 90 95

Glu Ser Gly Pro Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys
100 105 110

Val Ala Asn Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro
115 120 125

Glu Gln Asn Leu Arg Asn Trp Glu Glu Ile Ile Pro Glu Val Gln Trp
130 135 140

Arg Arg Ile Glu Gly Xaa Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr
145 150 155 160

Met Leu Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn Gly
165 170 175

Asn Glu Gly Arg Cys Ser Arg Ser Arg Arg Tyr Ser Gly Ser Asp Ser

180	185	190
Asp Ser Ile Ser Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg		
195	200	205
Thr Ile Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg		
210	215	220
Arg Phe Ile Lys Ser Tyr Lys Lys Phe Gly Gly Pro Val Glu Arg Leu		
225	230	235
240		
Asp Ala Ile Ala Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp		
245	250	255
Leu Arg Arg Leu Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu		
260	265	270
Asn Asp Asn Asp Phe Gly Gln Gly Arg Thr Gly Gly Arg Phe Gly Lys		
275	280	285
Val Lys Gly Pro Thr Phe Arg Ile Ala Gly Val Gln Val Asn Ala Lys		
290	295	300
Leu Val Ile Ser His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile		
305	310	315
320		
Pro Ser Asp Pro Glu Glu Arg Lys Arg Tyr Val Ile Pro Tyr His Thr		
325	330	335
Lys Ala Ala His Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn		
340	345	350
Leu Leu Ile Gly Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile		
355	360	365
Lys Met Asp Pro Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp		
370	375	380

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Pro Asp Lys Lys Pro Gln Ala Lys Gln Leu Gln Thr Arg Ala Asp Tyr
385 390 395 400
Leu Ile Lys Leu Leu Asn Lys Asp Leu Ala Arg Lys Glu Ala Gln Arg
405 410 415
Leu Ala Gly Ala Gly Asn Ser Lys Arg Arg Lys Thr Arg Ser Lys Lys
420 425 430
Asn Lys Ala Thr Lys Ala Ala
435

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1434 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..1434

(D) OTHER INFORMATION:/note= "The sequence beginning at 1

corresponds to 55 and that ending at 1434 corresponds to

1488"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Lys Pro Pro Lys Ala Asp Gly Ser Glu Phe Trp Lys Ser Ser Pro Ser
1 5 10 15

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Ile	Leu	Ala	Val	Gln	Arg	Ser	Ala	Val	Leu	Lys	Lys	Gln	Gln	Gln	Gln
			20					25					30		
Gln	Lys	Ala	Ala	Ser	Ser	Asp	Ser	Gly	Ser	Glu	Glu	Asp	Ser	Ser	Ser
		35					40					45			
Ser	Glu	Asp	Ser	Ala	Asp	Asp	Ser	Ser	Ser	Glu	Thr	Lys	Lys	Lys	Lys
	50					55				60					
His	Lys	Asp	Glu	Asp	Trp	Gln	Met	Ser	Gly	Ser	Gly	Ser	Val	Ser	Gly
65					70					75				80	
Thr	Gly	Ser	Asp	Ser	Glu	Ser	Ala	Glu	Asp	Gly	Asp	Lys	Ser	Ser	Cys
			85					90					95		
Glu	Glu	Ser	Glu	Ser	Asp	Tyr	Glu	Pro	Lys	Asn	Lys	Val	Lys	Ser	Arg
		100					105					110			
Lys	Pro	Pro	Ser	Arg	Ile	Lys	Pro	Lys	Ser	Gly	Lys	Lys	Ser	Thr	Gly
	115					120						125			
Gln	Lys	Lys	Arg	Gln	Leu	Asp	Ser	Ser	Glu	Glu	Glu	Glu	Asp	Asp	Asp
	130					135						140			
Glu	Asp	Tyr	Asp	Lys	Arg	Gly	Ser	Arg	Arg	Gln	Ala	Thr	Val	Asn	Val
145					150					155				160	
Ser	Tyr	Lys	Glu	Ala	Glu	Glu	Thr	Lys	Thr	Asp	Ser	Asp	Asp	Leu	Leu
			165						170				175		
Glu	Val	Cys	Gly	Glu	Asp	Val	Pro	Gln	Thr	Glu	Glu	Asp	Glu	Phe	Glu
		180						185				190			
Thr	Ile	Glu	Lys	Phe	Met	Asp	Ser	Arg	Ile	Gly	Arg	Lys	Gly	Ala	Thr
	195						200					205			
Gly	Ala	Ser	Thr	Thr	Ile	Tyr	Ala	Val	Glu	Ala	Asp	Gly	Asp	Pro	Asn

210	215	220
Ala Gly Phe Glu Lys Ser Lys Glu Leu Gly Glu Ile Gln Tyr Leu Ile		
225	230	235
Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu		240
	245	250
Thr Leu Lys Gln Gln Asn Val Lys Gly Met Asn Lys Leu Asp Asn Tyr		255
	260	265
Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro		270
	275	280
Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu		285
	290	295
His Lys Gln Tyr Gln Ile Val Glu Arg Ile Ile Ala His Ser Asn Gln		300
305	310	315
Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu		320
	325	330
Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ala Lys Lys		335
	340	345
Phe Gln Ala Arg Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr		350
	355	360
Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val		365
	370	375
Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Ser Leu Glu		380
385	390	395
Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp		400
	405	410
		415

Cys	Lys	Gly	Asn	Ser	Cys	Ile	Leu	Ala	Asp	Glu	Met	Gly	Leu	Gly	Lys
			420					425					430		
Thr	Ile	Gln	Thr	Ile	Ser	Phe	Leu	Asn	Tyr	Leu	Phe	His	Glu	His	Gln
			435					440					445		
Leu	Tyr	Gly	Pro	Phe	Leu	Leu	Arg	Val	Pro	Leu	Ser	Thr	Leu	Thr	Ser
			450					455					460		
Trp	Gln	Arg	Glu	Ile	Gln	Thr	Trp	Ala	Pro	Gln	Met	Asn	Ala	Val	Val
			465					470					475		480
Tyr	Leu	Gly	Asp	Ile	Thr	Ser	Arg	Asn	Met	Ile	Arg	Thr	His	Glu	Trp
								485					490		495
Met	His	Pro	Gln	Thr	Lys	Arg	Leu	Lys	Phe	Asn	Ile	Leu	Leu	Thr	Thr
								500					505		510
Tyr	Glu	Ile	Leu	Leu	Lys	Asp	Lys	Ser	Phe	Leu	Gly	Gly	Leu	Asn	Trp
								515					520		525
Ala	Phe	Ile	Gly	Val	Asp	Glu	Ala	His	Arg	Leu	Lys	Asn	Asp	Asp	Ser
								530					535		540
Leu	Leu	Tyr	Arg	Thr	Leu	Ile	Asp	Phe	Lys	Ser	Asn	His	Arg	Leu	Leu
								545					550		555
Ile	Thr	Gly	Thr	Pro	Leu	Gln	Asn	Ser	Leu	Lys	Glu	Leu	Trp	Ser	Leu
								565					570		575
Leu	His	Phe	Ile	Met	Pro	Glu	Lys	Phe	Ser	Ser	Trp	Glu	Asp	Phe	Glu
								580					585		590
Glu	Glu	His	Gly	Lys	Gly	Arg	Glu	Tyr	Gly	Tyr	Ala	Ser	Leu	His	Lys
								595					600		605
Glu	Leu	Glu	Pro	Phe	Leu	Leu	Arg	Arg	Val	Lys	Lys	Asp	Val	Glu	Lys

610	615	620
Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala		
625	630	635
Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala		
645	650	655
Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met		
660	665	670
Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro		
675	680	685
Asp Asp Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile		
690	695	700
Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu		
705	710	715
Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met		
725	730	735
Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln		
740	745	750
Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp		
755	760	765
His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr		
770	775	780
Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val		
785	790	795
Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala		
805	810	815

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Arg	Ala	His	Arg	Ile	Gly	Gln	Lys	Lys	Gln	Val	Asn	Ile	Tyr	Arg	Leu
820				825				830							
Val	Thr	Lys	Gly	Ser	Val	Glu	Glu	Asp	Ile	Leu	Glu	Arg	Ala	Lys	Lys
835				840				845							
Lys	Met	Val	Leu	Asp	His	Leu	Val	Ile	Gln	Arg	Met	Asp	Thr	Thr	Gly
850				855				860							
Lys	Thr	Val	Leu	His	Thr	Gly	Ser	Thr	Pro	Ser	Ser	Ser	Thr	Pro	Phe
865				870				875				880			
Asn	Lys	Glu	Glu	Leu	Ser	Ala	Ile	Leu	Lys	Phe	Gly	Ala	Glu	Glu	Leu
885				890				895							
Phe	Lys	Glu	Pro	Glu	Gly	Glu	Glu	Gln	Glu	Pro	Gln	Glu	Met	Asp	Ile
900				905				910							
Asp	Glu	Ile	Leu	Lys	Arg	Ala	Glu	Thr	Arg	Glu	Asn	Glu	Pro	Gly	Pro
915				920				925							
Leu	Thr	Val	Gly	Asp	Glu	Leu	Leu	Ser	Gln	Phe	Lys	Val	Ala	Asn	Phe
930				935				940							
Ser	Asn	Met	Asp	Glu	Asp	Asp	Ile	Glu	Leu	Glu	Pro	Glu	Arg	Asn	Ser
945				950				955				960			
Arg	Asn	Trp	Glu	Glu	Ile	Ile	Pro	Glu	Ser	Gln	Arg	Arg	Arg	Ile	Glu
965				970				975							
Glu	Glu	Glu	Arg	Gln	Lys	Glu	Leu	Glu	Glu	Ile	Tyr	Met	Leu	Pro	Arg
980				985				990							
Met	Arg	Asn	Cys	Ala	Lys	Gln	Ile	Ser	Phe	Asn	Gly	Ser	Glu	Gly	Arg
995				1000				1005							
Arg	Ser	Arg	Ser	Arg	Arg	Tyr	Ser	Gly	Ser	Asp	Ser	Asp	Ser	Ile	Thr

1010	1015	1020
Glu Arg Lys Arg Pro Lys Lys Arg Gly Arg Pro Arg Thr Ile Pro Arg		
1025	1030	1035
Glu Asn Ile Lys Gly Phe Ser Asp Ala Glu Ile Arg Arg Phe Ile Lys		1040
	1045	1050
Ser Tyr Lys Lys Phe Gly Gly Pro Leu Glu Arg Leu Asp Ala Val Ala		1055
	1060	1065
Arg Asp Ala Glu Leu Val Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu		1070
	1075	1080
Gly Glu Leu Val His Asn Gly Cys Ile Lys Ala Leu Lys Asp Asn Ser		1085
	1090	1095
Ser Gly Gln Glu Arg Ala Gly Gly Arg Leu Gly Lys Val Lys Gly Pro		1100
1105	1110	1115
Thr Phe Arg Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ser		1120
	1125	1130
His Glu Glu Glu Leu Ala Pro Leu His Lys Ser Ile Pro Ser Asp Pro		1135
	1140	1145
Glu Glu Arg Lys Arg Tyr Val Ile Pro Cys His Thr Lys Ala Ala His		1150
	1155	1160
Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Val Gly		1165
	1170	1175
Ile Tyr Glu Tyr Gly Tyr Gly Ser Trp Glu Met Ile Lys Met Asp Pro		1180
1185	1190	1195
Asp Leu Ser Leu Thr Gln Lys Ile Leu Pro Asp Asp Pro Asp Lys Lys		1200
	1205	1210
		1215

Pro	Gln	Ala	Lys	Gln	Leu	Gln	Thr	Arg	Ala	Asp	Tyr	Leu	Ile	Lys	Leu
1220				1225				1230							
Leu	Asn	Lys	Asp	Leu	Ala	Arg	Lys	Glu	Ala	Gln	Arg	Leu	Ala	Gly	Ala
1235				1240				1245							
Gly	Asn	Ser	Lys	Arg	Arg	Lys	Thr	Arg	Asn	Lys	Lys	Asn	Lys	Met	Lys
1250				1255				1260							
Ala	Ser	Lys	Ile	Lys	Glu	Glu	Ile	Lys	Ser	Asp	Ser	Ser	Pro	Gln	Pro
1265				1270				1275				1280			
Ser	Glu	Lys	Ser	Asp	Glu	Asp	Asp	Glu	Glu	Glu	Asp	Asn	Lys	Val	Asn
1285				1290				1295							
Glu	Met	Lys	Ser	Glu	Asn	Lys	Glu	Lys	Ser	Lys	Lys	Ile	Pro	Leu	Leu
1300				1305				1310							
Asp	Thr	Pro	Val	His	Ile	Thr	Ala	Thr	Ser	Glu	Pro	Val	Pro	Ile	Ser
1315				1320				1325							
Glu	Glu	Ser	Glu	Glu	Leu	His	Gln	Lys	Thr	Phe	Ser	Val	Cys	Lys	Glu
1330				1335				1340							
Arg	Met	Arg	Pro	Val	Lys	Ala	Ala	Leu	Lys	Gln	Leu	Asp	Arg	Pro	Glu
1345				1350				1355				1360			
Lys	Gly	Leu	Ser	Glu	Arg	Glu	Gln	Leu	Glu	His	Thr	Arg	Gln	Cys	Leu
1365				1370				1375							
Ile	Lys	Ile	Gly	Asp	His	Ile	Thr	Glu	Cys	Leu	Lys	Glu	Tyr	Thr	Asn
1380				1385				1390							
Pro	Glu	Gln	Ile	Lys	Gln	Trp	Arg	Lys	Asn	Leu	Trp	Ile	Phe	Val	Ser
1395				1400				1405							
Lys	Phe	Thr	Glu	Phe	Asp	Ala	Arg	Lys	Leu	His	Lys	Leu	Tyr	Lys	His

1410	1415	1420
Ala Ile Lys Lys Arg Gln Glu Ser Gln Gln		
1425	1430	

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1467 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:1..1467

(D) OTHER INFORMATION:/note= "The sequence beginning at 1

corresponds to 2654 and that ending at 1467 corresponds to

4120"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Ala Ala Lys Asp Ile Ser Thr Glu Val Leu Gln Asn Pro Glu Leu

1 5 10 15

Tyr Gly Leu Arg Arg Ser His Arg Ala Ala Ala His Gln Gln Asn Tyr

20 25 30

Phe Asn Asp Ser Asp Asp Glu Asp Asp Glu Asp Asn Ile Lys Gln Ser

35 40 45

Arg Arg Lys Arg Met Thr Thr Ile Glu Asp Asp Glu Asp Glu Phe Glu

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50						55						60			
Asp	Glu	Glu	Gly	Glu	Glu	Asp	Ser	Gly	Glu	Asp	Glu	Asp	Glu	Glu	Asp
65						70						75			80
Phe	Glu	Glu	Asp	Asp	Asp	Tyr	Tyr	Gly	Ser	Pro	Ile	Lys	Gln	Asn	Arg
						85						90			95
Ser	Lys	Pro	Lys	Ser	Arg	Thr	Lys	Ser	Lys	Ser	Lys	Ser	Lys	Pro	Lys
						100						105			110
Ser	Gln	Ser	Glu	Lys	Gln	Ser	Thr	Val	Lys	Ile	Pro	Thr	Arg	Phe	Ser
						115						120			125
Asn	Arg	Gln	Asn	Lys	Thr	Val	Asn	Tyr	Asn	Ile	Asp	Tyr	Ser	Asp	Asp
						130						135			140
Asp	Leu	Leu	Glu	Ser	Glu	Asp	Asp	Tyr	Gly	Ser	Glu	Glu	Ala	Leu	Ser
145						150						155			160
Glu	Glu	Asn	Val	His	Glu	Ala	Ser	Ala	Asn	Pro	Gln	Pro	Glu	Asp	Phe
						165						170			175
His	Gly	Ile	Asp	Ile	Val	Ile	Asn	His	Arg	Leu	Lys	Thr	Ser	Leu	Glu
						180						185			190
Glu	Gly	Lys	Val	Leu	Glu	Lys	Thr	Val	Pro	Asp	Leu	Asn	Asn	Cys	Lys
						195						200			205
Glu	Asn	Tyr	Glu	Phe	Leu	Ile	Lys	Trp	Thr	Asp	Glu	Ser	His	Leu	His
						210						215			220
Asn	Thr	Trp	Glu	Thr	Tyr	Glu	Ser	Ile	Gly	Gln	Val	Arg	Gly	Leu	Lys
225						230						235			240
Arg	Leu	Asp	Asn	Tyr	Cys	Lys	Gln	Phe	Ile	Ile	Glu	Asp	Gln	Gln	Val
						245						250			255

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Arg	Leu	Asp	Pro	Tyr	Val	Thr	Ala	Glu	Asp	Ile	Glu	Ile	Met	Asp	Met
260				265				270							
Glu	Arg	Glu	Arg	Arg	Leu	Asp	Glu	Phe	Glu	Glu	Phe	His	Val	Pro	Glu
275				280				285							
Arg	Ile	Ile	Asp	Ser	Gln	Arg	Ala	Ser	Leu	Glu	Asp	Gly	Thr	Ser	Gln
290				295				300							
Leu	Gln	Tyr	Leu	Val	Lys	Trp	Arg	Arg	Leu	Asn	Tyr	Asp	Glu	Ala	Thr
305				310				315				320			
Trp	Glu	Asn	Ala	Thr	Asp	Ile	Val	Lys	Leu	Ala	Pro	Glu	Gln	Val	Lys
325				330				335							
His	Phe	Gln	Asn	Arg	Glu	Asn	Ser	Lys	Ile	Leu	Pro	Gln	Tyr	Ser	Ser
340				345				350							
Asn	Tyr	Thr	Ser	Gln	Arg	Pro	Arg	Phe	Glu	Lys	Leu	Ser	Val	Gln	Pro
355				360				365							
Pro	Phe	Ile	Lys	Gly	Gly	Glu	Leu	Arg	Asp	Phe	Gln	Leu	Thr	Gly	Ile
370				375				380							
Asn	Trp	Met	Ala	Phe	Leu	Trp	Ser	Lys	Gly	Asp	Asn	Gly	Ile	Leu	Ala
385				390				395				400			
Asp	Glu	Met	Gly	Leu	Gly	Lys	Thr	Val	Gln	Thr	Val	Ala	Phe	Ile	Ser
405				410				415							
Trp	Leu	Ile	Phe	Ala	Arg	Arg	Gln	Asn	Gly	Pro	His	Ile	Ile	Val	Val
420				425				430							
Pro	Leu	Ser	Thr	Met	Pro	Ala	Trp	Leu	Asp	Thr	Phe	Glu	Lys	Trp	Ala
435				440				445							
Pro	Asp	Leu	Asn	Cys	Ile	Cys	Tyr	Met	Gly	Asn	Gln	Lys	Ser	Arg	Asp

450		455		460											
Thr	Ile	Arg	Glu	Tyr	Glu	Phe	Tyr	Thr	Asn	Pro	Arg	Ala	Lys	Gly	Lys
465				470				475						480	
Lys	Thr	Met	Lys	Phe	Asn	Val	Leu	Leu	Thr	Thr	Tyr	Glu	Tyr	Ile	Leu
			485					490						495	
Lys	Asp	Arg	Ala	Glu	Leu	Gly	Ser	Ile	Lys	Trp	Gln	Phe	Met	Ala	Val
		500						505					510		
Asp	Glu	Ala	His	Arg	Leu	Lys	Asn	Ala	Glu	Ser	Ser	Leu	Tyr	Glu	Ser
		515						520					525		
Leu	Asn	Ser	Phe	Lys	Val	Ala	Asn	Arg	Met	Leu	Ile	Thr	Gly	Thr	Pro
	530						535					540			
Leu	Gln	Asn	Asn	Ile	Lys	Glu	Leu	Ala	Ala	Leu	Val	Asn	Phe	Leu	Met
545					550					555				560	
Pro	Gly	Arg	Phe	Thr	Ile	Asp	Gln	Glu	Ile	Asp	Phe	Glu	Asn	Gln	Asp
			565							570				575	
Glu	Glu	Gln	Glu	Glu	Tyr	Ile	His	Asp	Leu	His	Arg	Arg	Ile	Gln	Pro
			580						585					590	
Phe	Ile	Leu	Arg	Arg	Leu	Lys	Lys	Asp	Val	Glu	Lys	Ser	Leu	Pro	Ser
		595						600					605		
Lys	Thr	Glu	Arg	Ile	Leu	Arg	Val	Glu	Leu	Ser	Asp	Val	Gln	Thr	Glu
	610							615					620		
Tyr	Tyr	Lys	Asn	Ile	Leu	Thr	Lys	Asn	Tyr	Ser	Ala	Leu	Thr	Ala	Gly
625					630					635				640	
Ala	Lys	Gly	Gly	His	Phe	Ser	Leu	Leu	Asn	Ile	Met	Asn	Glu	Leu	Lys
			645							650				655	

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Lys	Ala	Ser	Asn	His	Pro	Tyr	Leu	Phe	Asp	Asn	Ala	Glu	Glu	Arg	Val
			660					665					670		
Leu	Gln	Lys	Phe	Gly	Asp	Gly	Lys	Met	Thr	Arg	Glu	Asn	Val	Leu	Arg
			675					680					685		
Gly	Leu	Ile	Met	Ser	Ser	Gly	Lys	Met	Val	Leu	Leu	Asp	Gln	Leu	Leu
			690					695					700		
Thr	Arg	Leu	Lys	Lys	Asp	Gly	His	Arg	Val	Leu	Ile	Phe	Ser	Gln	Met
705								710					715		720
Val	Arg	Met	Leu	Asp	Ile	Leu	Gly	Asp	Tyr	Leu	Ser	Ile	Lys	Gly	Ile
								725					730		735
Asn	Phe	Gln	Arg	Leu	Asp	Gly	Thr	Val	Pro	Ser	Ala	Gln	Arg	Arg	Ile
								740					745		750
Ser	Ile	Asp	His	Phe	Asn	Ser	Pro	Asp	Ser	Asn	Asp	Phe	Val	Phe	Leu
								755					760		765
Leu	Ser	Thr	Arg	Ala	Gly	Gly	Leu	Gly	Ile	Asn	Leu	Met	Thr	Ala	Asp
								770					775		780
Thr	Val	Val	Ile	Phe	Asp	Ser	Asp	Trp	Asn	Pro	Gln	Ala	Asp	Leu	Gln
785								790					795		800
Ala	Met	Ala	Arg	Ala	His	Arg	Ile	Gly	Gln	Lys	Asn	His	Val	Met	Val
								805					810		815
Tyr	Arg	Leu	Val	Ser	Lys	Asp	Thr	Val	Glu	Glu	Glu	Val	Leu	Glu	Arg
								820					825		830
Ala	Arg	Lys	Lys	Met	Ile	Leu	Glu	Tyr	Ala	Ile	Ile	Ser	Leu	Gly	Val
								835					840		845
Thr	Asp	Gly	Asn	Lys	Tyr	Thr	Lys	Lys	Asn	Glu	Pro	Asn	Ala	Gly	Glu

850	855	860
Leu Ser Ala Ile Leu Lys Phe Gly Ala Gly Asn Met Phe Thr Ala Thr		
865	870	875
Asp Asn Gln Lys Lys Leu Glu Asp Leu Asn Leu Asp Asp Val Leu Asn		880
	885	890
His Ala Glu Asp His Val Thr Thr Pro Asp Leu Gly Glu Ser His Leu		895
	900	905
Gly Gly Glu Glu Phe Leu Lys Gln Phe Glu Val Thr Asp Tyr Lys Ala		910
	915	920
Asp Ile Asp Trp Asp Asp Ile Ile Pro Glu Glu Glu Leu Lys Lys Leu		925
	930	935
Gln Asp Glu Glu Gln Lys Arg Lys Asp Glu Glu Tyr Val Lys Glu Gln		940
945	950	955
Leu Glu Met Met Asn Arg Arg Asp Asn Ala Leu Lys Lys Ile Lys Asn		960
	965	970
Ser Val Asn Gly Asp Gly Thr Ala Ala Asn Ser Asp Ser Asp Asp Asp		975
	980	985
Ser Thr Ser Arg Ser Ser Arg Arg Arg Ala Arg Ala Asn Asp Met Asp		990
	995	1000
Ser Ile Gly Glu Ser Glu Val Arg Ala Leu Tyr Lys Ala Ile Leu Lys		1005
	1010	1015
Phe Gly Asn Leu Lys Glu Ile Leu Asp Glu Leu Ile Ala Asp Gly Thr		1020
1025	1030	1035
Leu Pro Val Lys Ser Phe Glu Lys Tyr Gly Glu Thr Tyr Asp Glu Met		1040
	1045	1050
		1055

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Met	Glu	Ala	Ala	Lys	Asp	Cys	Val	His	Glu	Glu	Glu	Lys	Asn	Arg	Lys
			1060						1065					1070	
Glu	Ile	Leu	Glu	Lys	Leu	Glu	Lys	His	Ala	Thr	Ala	Tyr	Arg	Ala	Lys
			1075						1080					1085	
Leu	Lys	Ser	Gly	Glu	Ile	Lys	Ala	Glu	Asn	Gln	Pro	Lys	Asp	Asn	Pro
			1090						1095					1100	
Leu	Thr	Arg	Leu	Ser	Leu	Lys	Lys	Arg	Glu	Lys	Lys	Ala	Val	Leu	Phe
1105									1110					1115	1120
Asn	Phe	Lys	Gly	Val	Lys	Ser	Leu	Asn	Ala	Glu	Ser	Leu	Leu	Ser	Arg
									1125					1130	1135
Val	Glu	Asp	Leu	Lys	Tyr	Leu	Lys	Asn	Leu	Ile	Asn	Ser	Asn	Tyr	Lys
									1140					1145	1150
Asp	Asp	Pro	Leu	Lys	Phe	Ser	Leu	Gly	Asn	Asn	Thr	Pro	Lys	Pro	Val
									1155					1160	1165
Gln	Asn	Trp	Ser	Ser	Asn	Trp	Thr	Lys	Glu	Glu	Asp	Glu	Lys	Leu	Leu
									1170					1175	1180
Ile	Gly	Val	Phe	Lys	Tyr	Gly	Tyr	Gly	Ser	Trp	Thr	Gln	Ile	Arg	Asp
1185									1190					1195	1200
Asp	Pro	Phe	Leu	Gly	Ile	Thr	Asp	Lys	Ile	Phe	Leu	Asn	Glu	Val	His
									1205					1210	1215
Asn	Pro	Val	Ala	Lys	Lys	Ser	Ala	Ser	Ser	Ser	Asp	Thr	Thr	Pro	Thr
									1220					1225	1230
Pro	Ser	Lys	Lys	Gly	Lys	Gly	Ile	Thr	Gly	Ser	Ser	Lys	Lys	Val	Pro
									1235					1240	1245
Gly	Ala	Ile	His	Leu	Gly	Arg	Arg	Val	Asp	Tyr	Leu	Leu	Ser	Phe	Leu

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1250	1255	1260
Arg Gly Gly Leu Asn Thr Lys Ser Pro Ser Ala Asp Ile Gly Ser Lys		
1265	1270	1275
Lys Leu Pro Thr Gly Pro Ser Lys Lys Arg Gln Arg Lys Pro Ala Asn		1280
	1285	1290
His Ser Lys Ser Met Thr Pro Glu Ile Thr Ser Ser Glu Pro Ala Asn		1295
	1300	1305
Gly Pro Pro Ser Lys Arg Met Lys Ala Leu Pro Lys Gly Pro Ala Ala		1310
	1315	1320
Leu Ile Asn Asn Thr Arg Leu Ser Pro Asn Ser Pro Thr Pro Pro Leu		1325
	1330	1335
Lys Ser Lys Val Ser Arg Asp Asn Gly Thr Arg Gln Ser Ser Asn Pro		1340
1345	1350	1355
Ser Ser Gly Ser Ala His Glu Lys Glu Tyr Asp Ser Met Asp Glu Glu		1360
	1365	1370
Asp Cys Arg His Thr Met Ser Ala Ile Arg Thr Ser Leu Lys Arg Leu		1375
	1380	1385
Arg Arg Gly Gly Lys Ser Leu Asp Arg Lys Glu Trp Ala Lys Ile Leu		1390
	1395	1400
Lys Thr Glu Leu Thr Thr Ile Gly Asn His Ile Glu Ser Gln Lys Gly		1405
	1410	1415
Ser Ser Arg Lys Ala Ser Pro Glu Lys Tyr Arg Lys His Leu Trp Ser		1420
1425	1430	1435
Tyr Ser Ala Asn Phe Trp Pro Ala Asp Val Lys Ser Thr Lys Leu Met		1440
	1445	1450
		1455

Ala Met Tyr Asp Lys Ile Thr Glu Ser Gln Lys

1460

1465

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Val Glu Ala Asp Gly Asp Pro Asn Ala Gly Phe Glu Lys Ser Lys

1 5 10 15

Glu Leu Gly Glu Ile Gln Tyr Leu Ile Lys Trp Lys Gly Trp Ser His

20 25 30

Ile His Asn Thr Trp Glu Thr Glu Glu Thr Leu Lys Gln Gln Asn Val

35 40 45

Lys Gly Met Asn Lys Leu Asp Asn Tyr Lys Lys

50

55

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Ala	Val	Glu	Ala	Asp	Gly	Asp	Pro	Asn	Ala	Gly	Phe	Glu	Arg	Asn	Lys
1				5					10					15	
Glu	Pro	Gly	Asp	Ile	Gln	Tyr	Leu	Ile	Lys	Trp	Lys	Gly	Trp	Ser	His
				20					25					30	
Ile	His	Asn	Thr	Trp	Glu	Thr	Glu	Glu	Thr	Leu	Lys	Gln	Gln	Asn	Val
				35					40					45	
Arg	Gly	Asn	Lys	Lys	Leu	Asp	Asn	Tyr	Lys	Lys					
				50					55						

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Glu	Gly	Lys	Val	Leu	Glu	Lys	Thr	Val	Pro	Asp	Leu	Asn	Asn	Cys	Lys
1				5					10					15	
Glu	Asn	Tyr	Glu	Phe	Leu	Ile	Lys	Trp	Thr	Asp	Glu	Ser	His	Leu	His
				20					25					30	
Asn	Thr	Trp	Glu	Thr	Tyr	Glu	Ser	Ile	Gly	Gln	Val	Arg	Gly	Leu	Lys

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35	40	45
Arg	Leu	Asp
Asn	Tyr	Cys
Lys		
50	55	

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Glu	Glu	Glu	Glu	Glu	Tyr	Ala	Val	Glu	Lys	Ile	Ile	Asp	Arg	Arg	Val
1				5					10					15	
Arg	Lys	Gly	Lys	Val	Glu	Tyr	Tyr	Leu	Lys	Trp	Lys	Gly	Tyr	Pro	Glu
				20				25					30		
Thr	Glu	Asn	Thr	Trp	Glu	Pro	Glu	Asn	Asn	Leu	Asp	Cys	Gln	Asp	Leu
				35				40					45		
Ile	Gln	Gln	Tyr												
				50											

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Asp Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val

1 5 10 15

Val Lys Gly Lys Gln Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser

20 25 30

Glu Glu His Asn Thr Trp Glu Pro Glu Lys Asn Leu Asp Cys Pro Glu

35 40 45

Leu Ile Ser Glu Phe

50

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Glu Glu Glu Glu Glu Tyr Val Val Glu Lys Val Leu Asp Arg Arg Val

1 5 10 15

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Val Lys Gly Lys Val Glu Tyr Leu Leu Lys Trp Lys Gly Phe Ser Asp
20 25 30
Glu Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Asp Leu
35 40 45
Ile Ala Glu Phe
50

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Ala Glu Pro Glu Glu Phe Val Val Glu Lys Val Leu Asp Arg Arg Val
1 5 10 15
Val Asn Gly Lys Val Glu Tyr Phe Leu Lys Trp Lys Gly Phe Thr Asp
20 25 30
Ala Asp Asn Thr Trp Glu Pro Glu Glu Asn Leu Asp Cys Pro Glu Leu
35 40 45
Ile Glu Asp Phe
50

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Pro	Val	Asp	Leu	Val	Tyr	Ala	Ala	Glu	Lys	Ile	Ile	Gln	Lys	Arg	Val
1				5					10					15	
Lys	Lys	Gly	Val	Val	Glu	Tyr	Arg	Val	Lys	Trp	Lys	Gly	Trp	Asn	Gln
				20				25						30	
Arg	Tyr	Asn	Thr	Trp	Glu	Pro	Glu	Asn	Asn	Ile	Leu	Asp	Arg	Arg	Leu
		35					40						45		
Ile	Asp	Ile	Tyr												
				50											

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Val Gly Glu Gln Val Phe Ala Ala Glu Cys Ile Leu Ser Lys Arg Leu
1 5 10 15
Arg Lys Gly Lys Leu Glu Tyr Leu Val Lys Trp Arg Gly Trp Ser Ser
 20 25 30
Lys His Asn Ser Trp Glu Pro Glu Glu Asn Ile Leu Asp Pro Arg Leu
 35 40 45
Leu Leu Ala Phe
 50

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AGATATTCTG GATCTGATAG TGATTCAATC TCGGAAAGGA AACGGCCGAA GAAACGTGGG 60
CGACCCCGCA CTATCCCTCG GGAGAATATT AAAGGATTTA GTGATGCGGA G 111

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AGATATTCTG GATCTGATAG TGA	CTCCATC ACAGAAAGAA AACGGCCAAA AAAGCGTGG	60
AGACCTCGAA CCATTCCTCG AGAAAATATT AAAGGATT	TA GTGATGCAGA G	111

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTCCATCTCG GAAAGGAAAC GGCCAAAAAA GCGTGGAAGA CCACGAACTA TTCCTCGAGA	60
AAATATA	67

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGATATTCTG GATCTGATAG TGATTCCATC TCAGAAAGAA AACGACCAAA AAAACGTGGA	60
CGACCACGAA CTATTCCCCG TGAAAACATT AAAGGATTTA GTGATGCAGA G	111

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTCCATCTCA GAAAGAAAAC GACCAAGAAA ACGTGGACGA CCACGAACTA TTCCTCGTGA	60
AAATATT	67

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GATCTGATAG TGA TCCATC TCAGAAAGAA AACGACCAAG AAAACGTGGA CGACCACGAA	60
CTATCCCTCG GGAGAATATT AAAGGATTTA GCGATGCAGA GATTAGGCGG T	111

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ATATTCTGGA TCTGATAGTG AYTC

24

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AGATATTCCG GATCTGATAG TGA

23

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic DNA Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TTTCCTAAAT CGCTACGTCT

20